

Changes in the Predicted Secondary Structure of Interleukin-2 mRNA Associated With Its CD28-Mediated Stabilization***Cole, Steven^{*1,2}, Kasprzak, Wojciech³, Shapiro, Bruce⁴, Ragheb, Jack²******¹George Mason University, Fairfax, VA, USA; ²LI, National Eye Institute, NIH, Bethesda, MD, USA; ³BRP, SAIC-Frederick, Inc., and ⁴LECB, National Cancer Institute at Frederick, Frederick, MD, USA***

Historically, mRNA secondary structure has been overlooked compared to its protein counterpart, however these structures are extremely active metabolically with numerous unique protein interactions. Signaling through the CD28 receptor stabilizes the Interlukin-2 (IL-2) mRNA. Traditional wet lab research has demonstrated that the second exon of the mRNA is necessary for this stabilization. We hypothesized that stabilization may be dependent on an interaction between the second exon and an unknown protein. A Genetic Algorithm (GA) implementation was used to generate possible secondary structures, which were further analyzed using Stem Trace, a tool from the STRUCTURELAB computer workbench, both developed at NCI's LECB. We have identified a potential hairpin-loop structure within exon 2 that may represent a binding site for such a protein. Further genetic and biochemical analyses of these sequences will be required to verify the physical existence and biological significance of this unique architecture in CD28-mediated IL-2 mRNA stabilization.